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GenCore version 4.5

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OM protein - protein search, using sw model

Run on:

August 21, 2001, 12:06:13; Search time 16.04 Seconds (without alignments) 1491.198 Million cell updates/sec

Title:
Sequence:

1641
Sequence:

1641
Sequence:

1642
Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:

219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

219241
Minimum DB seq length: 0
Maximum B seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

## SUMMARIES

2,4	2 6	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	5	4	ω	N	1	Result
ä		·ω			409	20	422.5			472.5							648.5				699		$\mathbf{a}$	~1	Ξ	21	_	~	Score
		23.9								•		•	•	•				•	•	•	•	•	•	•	67.3	•	•	•	Query Match
212	199	258	229	229	251	249	227	217	225	270	261	274	299	267	308	273	273	273	273	272	315	312	294	347	303	391	314	314	Length
Ν.	N	2	N	Ν	N	Ц	N	Н	۳	2	Н	N	N	N	N	N	2	N	r	N	N	N	N	N	N	N	N	2	DB
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RESULT S71181

44	43	42	41	40	39	38 8	37	36	ა <b>5</b>	34	ω <b>G</b>	3 <b>2</b>	31	30
171 $164.5$	175	175	177.5	179	207	217	217	265	287	312	338.5	359	365	369.5
10.4	10.7	10.7	10.8	10.9	12.6	13.2	13.2	16.1	17.5	19.0	20.6	21.9	22.2	22.5
190	240	236	143	256	184	162	162	231	319	171	220	171	171	269
NN	N	N	2	N	N	N	Ν	N	Ν	2	2	N	μ	ш
S07000	E83983	H72245	G82264	A86660	C82264	B85832	A64972	H83381	S55322	D84302	G72349	B71845	B64671	D43706
nypothetical prote nodulation protein	tetrahydrodipicoli	2,3,4,5-tetrahydro	serine acetyltrans	acetyltransferase	serine acetyltrans	probable transfera	probable acetyl tr	probable acetyltra	srpH protein - Syn	serine acetyltrans	serine acetyltrans	o-serine acetyltra	serine O-acetyltra	serine O-acetyltra

## ALIGNMENTS

RESULT S67482

	Db 301 DQTSYLTEMSDYVI 314	-
	Qy 301 DQTSYLTEWSDYVI 314	~
	Db 241 IGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM 300	_
	Qy 241 IGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM 300	_
	Db 181 VDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVL 240	
	Qy 181 VDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVL 240	_
	Db 121 KQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFA 180	_
	QY 121 KQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLMKQNRKIVALLIQNRVSESFA 180	_
	Db 61 KQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIEST 120	
	QY 61 KQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIEST 120	~
	Db 1 MATCIDTCRTGNTQDDDSRFCCIKNFTRPGFSVNRKIHHTQIEDDDDVWIKMLEEAKSDV 60	_
	OY 1 MATCIDTCRTGNTQDDDSRFCCIKNFFRPGFSVNRKIHHTQIEDDDDVWIKMLEEAKSDV 60	_
0;	Query Match 100.0%; Score 1641; DB 2; Length 314; Best Local Similarity 100.0%; Pred. No. 8.8e-129; Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps	
	C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis F;123-283/Domain: serine acetyltransferase homology <sat></sat>	<b>#</b> 0
A for resid	A; Note: the authors translated the codon ACC for residue 158 as Ile and ACA C; Superfamily: serine acetyltransferase; serine acetyltransferase homology	o *∗
	A; restaues: 1-314 <rus> A; Cross-references: EMBL:Z34888; NID:g608676; PIDN:CAA84371.1; PID:g608677</rus>	~ ~
	A; Molecule type: DNA	. ~ .
	A;Reference number: S67482; MUID:95154333 A:Accession: S67482	~ ~
tivum and	Eur. J. Blochem. 227, 500-509, 1995 A;Title: Subcellular distribution of serine acetyltransferase from Pisum sativum and	~ =
	R; Ruffet, M.L.; Lebrun, M.; Droux, M.; Douce, R.	<b>m</b> (
0	C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000	
	N;Alternate names: serine acetyltransferase C;Species: Arabidopsis thaliana (mouse-ear cress)	O 7
	serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana	ro r

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A; Molecule type: mRNA
A; Residues: 1-391 <ROB>
A; Cross-references: EMBL:U22
A; Cross-references: EMBL Data L
A; Reference number: S71906
A; Accession: S71906
A; Molecule type: mRNA
A; Residues: 80-391 <HEL>
A; Cross-references: EMBL:X82
C; Genetics:
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C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-Mc; Accession: S71181
R; Murillo, M.; Foglia, R.; Diller, A.; Leustek, T.
submitted to the EMBL Data Library, August 1995
A; Description: Analysis of a cDNA encoding serine acetyltransferase
                                                                                                                                                                                                                                                                                                             R;Roberts, M.A.; Wray, J.L.
Plant Mol. Biol. 30, 1041-1049, 1996
A;Title: Cloning and characterisation of an A;Reference number: S69192; MUID:96270381
A;Accession: S69192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L42212; NID:g926938; PIDN:AAC37474.1; PID:g926939
A;Note: probably chloroplast isoform; no transit peptide given
C;Genetics:
A;Genome: nuclear
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; chloroplast; coenzyme A; cysteine biosynthesis
F;123-283/Domain: serine acetyltransferase homology <SAT>
A; Genome:
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C;Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 05-May-2000
C;Accession: S69192; S71906
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A; Residues: 1-314 < MUR>
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A; Accession: S71181
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Species: Arabidopsis thaliana (mouse-ear cress)
Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000
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                                                                EMBL: X82888; NID: g897677; PIDN: CAA58061.1; PID: g897678
                                                                                                                                                                                                                                        EMBL: U22964; NID: g1184047;
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98.1%;
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A;Gene: satA
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis F;113-272/Domain: serine acetyltransferase homology <SAT>
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F;61-391/Product: serine O-acetyltransferase SAT-la, chloroplast #status predicted F;200-360/Domain: serine acetyltransferase homology <SAT>
                Qγ
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
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A; Residues: 1-303 < BOG>
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132 PACISYVHCELGEKGELACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPGAKIGK 191
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                                                                                             ASITSHRSLESALAHILSYKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERD 131
                                                                                                                                      NYFRYPDRSSFNGTQTKTLHTRPLLEDLDRDAEVDDVWAKIREEAKSDIAKEPIVSAYYH
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73.0%;
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72.0%;
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                                                                                                                                                                                                                                       Score 1105; DB 2; Pred. No. 2.8e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1215; DB 2; Pred. No. 2.9e-93;
                                                                                                                                                                                                                    Mismatches
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PACISYVHCFLHFKGFLACQAHRIAHELWTQDRKILALLIQNRVSEAFAVDFHPGAKIGT

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A;Experimental source: leaf C;Function:
C;Function:
A;Description: catalyzes conversion of L-serine to O-acetyl serine A;Description: catalyzes conversion of L-serine to O-acetyl serine A;Pathway: cysteine biosynthesis
C;Superfamily: serine acetyltransferase; serine acetyltransferase h
C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
E;156-316/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Spinacia oleracea (spinach)
C;Date: 11-Jun-1999 #sequence_revision
C;Accession: T09110
R;Saito, K; Takagi, Y.
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C;Species: Citrullus lanatus (watermelon)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-19
C;Accession: A57478
R;Saito, K.; Yokoyama, H.; Noji, M.; Murakoshi,
J. Biol. Chem. 270, 16321-16326, 1995
A;Title: Molecular cloning and characterization
A;Reference number: A57478; MUID:95332343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
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A; Residues: 1-347 <SAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, October 1996 A; Description: A cDNA encoding serine acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine O-acetyltransferase (EC 2.3.1.30) - spinach N;Alternate names: serine acetyltransferase
                                                                                                                             serine O-acetyltransferase (EC 2.3.1.30) - watermelon C; Species: Citrullus lanatus (watermelon)
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A57478
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                                                                                                                                                                                                                                                              IDVPPRTTAVGNPARLIGGKEKPSQNSDVPGESMDHTSFISEWSDYII 347
                                                                                                                                                                                                                                                                                                   KDVPARTTAVGNPARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                               ATTGDNCSTLHHVTLGGTGKAGGDRHPKVGDGVLTGAGATTLGNVRTGDGAKTGAGSVVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PG--FSVNRKIHHTQIEDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAH 86
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Pred. No. 2.9e-65;
3; Mismatches 70;
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A;Cross-references: GB:D49535; NID:q1060871; PIDN:BAA08479.1; PID:q1841312 C;Superfamily: serine acetyltransferase; serine acetyltransferase homology C;Keywords: acyltransferase; coenzyme A F;103-263/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A57478;
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-294 <SAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-312 <HOW>
A;Residues: 1-312 <HOW>
A;Cross-references: EMBL:U30298; NID:g905390; PIDN:AAC49655.1; PID:g905391
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
F;120-280/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              serine O-acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-C;Accession: S71207
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A; Accession: S71207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNPARLYGGKEKPSQLEDIPGESMDHTSFISEWSDYII 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNPARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIA 156
                                       SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHVTLGGTGKMCGDRHPKIGDGVLIGAGATILGNVKIGEGAKIGAGSVVLIDVPPRTTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGYTLGGTGKQSGDRHPKIGDGYLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKLWNQSRRPLALALQSRIADVFAYDIHPAARIGKGILFDHATGVVVGETAVIGNNVSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTLWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSIL
CGDRHPKIGDGCLIGAGATILGNVKIGAGAKVGAGSVVLIDVPCRGTAVGNPARLVGGKE
                                                                                       ALALHSRISDVFAVDIHPAAKIGKGILLDHATGVVVGETAVIGNNVSILHHVTLGGTGKA
                                                                                                            ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ 227
                                                                                                                                                                               NTFSSDPSLRNATVADLRAARVRDPACISFSHCLLNYKGFLAIQAHRVSHKLWTQSRKPL
                                                                                                                                                                                                                      SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
                                                                                                                                                                                                                                                                     LWTQIKAEARRDAEAEPALASYLYSTILSHSSLERSISFHLGNKLCSSTLLSTLLYDLFL
                                                                                                                                                                                                                                                                                                            VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLSTLLYDLFLNAFSTDYCLRSAVVADLQAARERDPACVSFSHCLLNYKGFLACQAHRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VESTINNDETWLWGQIKAEARRDAESEPALASYLYSTILSHSSLERSLSFHLGNKLCSST
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                                                                                                                                                                                                                                                                                                                                                          160;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts, M.A.; Wray, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 51.8%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                            45;
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Pred. No. 1.1e-64;
                                                                                                                                                                                                                                                                                                                                                          Score 849.5; DB 1
Pred. No. 4.9e-63;
5; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plants: a
                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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A;Cross-references: GB:AE002412; GB:AE002098; NID:g7225783; PIDN:AAF40988.1; PID:g722578A;Experimental source: serogroup B, strain MC58R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
                                                                                                                                                                                                                                                                                                                                   R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, F. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755
                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-272 <TET>
                                                                                                                                                                                                                                                                                                     A; Reference number: A81000; A; Accession: C81184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable serine O-acetyltransferase (EC 2.3.1.30) NMA0742 [imported] - Neis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: C81184; H81917
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A;Map position: 2
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A;Accession: F84554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable serine
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'Species: Arabidopsis thaliana (mouse-ear cress)

Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 AAGSLVLKDVPSHSVVAGNPAKLIRVME-----EQDPSLAM
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erty, B.A.
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A;Molecule type: DNA
A;Residues: 1-273 <PLU>
A;Residues: 1-273 <PLU>
A;Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18584.1; PID:g466745
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M15745; NID:g145675; PIDN:AAA23648.1; PID:g145676 R;Tei, H.; Murata, K.; Kimura, A. Biochem. Biophys. Res. Commun. 167, 948-955, 1990 A;Title: Structure and expression of CYSX, the second gene in the Escher A;Reference number: A34563; MUID:90211342 A;Accession: A34563
                                                                                                                                           R; Plunkett, G. submitted to the EMBL Data A; Reference number: S47666 A; Accession: S47828
                                                                                                                                                                                                                              A;Cross-references: GB:M34333; NID:g145693; PIDN:AAA23659.1; R;Plunkett, G.
                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-273 <TEI>
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A; Residues: 1-273 <DEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: L-Cysteine biosynthesis in Escherichia coli: nucleotide sequence and A;Reference number: A27896; MUID:88009872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Denk, D.; Bock, A.
J. Gen. Microbiol. 133, 515-525, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
C;Accession: A27896; A34563; S47828; A65161
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C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A
F;88-248/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A27896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Escherichia coli
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A; Residues: 1-272 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 VALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK
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hes 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLWHTIREETAAAVSAEPMLASFLHQTVLRHESLGSVLAYHLSSKLGSPIMDVRALFEIY
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Riley,

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serine O-acetyltransferase (EC 2.3.1.30) - Salmonella typhimurium C;Species: Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000 C;Accession: S29568
R;Sivaprasad, A.V.; Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.
submitted to the EMBL Data Library, May 1991
A;Description: A novel biosynthetic pathway for mammalian cells by stable integration of A;Reference number: S29567
A;Accession: S29567
A;Accession: S29568
A;Molecule type: DNA
A;Residues: 1-273 <SIV>
A;Cross-references: EMBL:X59594; NID:g47659; PIDN:CAA42163.1; PID:g47660
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
C;Keywords: acyltransferase; coenzyme A
F;84-244/Domain: serine acetyltransferase homology <SAT>
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A;Molecule type: DNA
A;Residues: 1-273 <BLAT>
A;Cross-references: GB:AE000438; GB:U00096; NID:g2267251; PIDN:AAC76631.1; PID:g1790035;
A;Cross-references: GB:AE000438; GB:U00096; NID:g2267251; PIDN:AAC76631.1; PID:g1790035;
A;Cross-references: GB:AE000438; GB:U00096; NID:g2267251; PIDN:AAC76631.1; PID:g1790035;
A;Comment: This enzyme catalyzes the conversion of L-serine to O-acetyl serine (by acetyl c;Cenetics:
A;Genetics:
A;Genetics:
A;Gene: CysE
A;Gene: CysE
A;Gene: GysE
A;Gene: 
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A;Accession: A65161
A;Status
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                                                                   FELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGKPDS----DK-PSMDMDQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG
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      REVVEEAYAADPEMTASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWNK 123
                                                                                                                                    EELEIVWKNIKAEARALADCEPMLASFYHATLLKHENLGSALSYMLANKLASPIMPAIAI 63
                                                                                                                                                                                                 EDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGGKENPRKHDKIPCLTMDQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTL 102
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                                                                                                                                                                                                                                                                     Score 648.5; DB Pred. No. 2e-46; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                               Length
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                                                             R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selll, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                              serine acetyltransferase VC2649 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Cate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: G82049
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio A; Reference number: A82035; MUID: 20406833
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A;Gene: cysE
C;Superfamily: serine acetyltransferase; serine acetyltransferase homology
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: F86036
C;Accession: Simple triangle of the collection of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-273 <STO>
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Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine acetyltransferase [imported] - Escherichia coli (strain 0157:H7)
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VGKPDS---
                                                            IGGKENPRKHDKIPCLTMDQ 302
                                                                                                                                                                                                    GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI
                                                                                                                                                                                                                                                                                                                                                                                                                   GRRALAIFLQNQVSVTFQVDIHPAAKIGRGIMLDHATGIVVGETAVIENDVSILQSVTLG
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submitted to the EMBL Data Library, October 1997
A; Reference number: Z16500
A; Accession: T08867
A; Scatus: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-308 <WAT>
A; Cross-references: EMBL:AF024504; NID:g2435510; PID:g2435513; GSPDB:GN00062; ATSP:A_TMCA; Experimental source: cultivar Columbia; BAC clone TM017A05
C; Genetics: A: Gene: ATSP:A_TM017A05.1
A; Map position: 4
A; Introns: 47/3; 113/3; 139/2; 181/1; 212/3; 273/2; 298/1
A; Introns: 47/3; 113/3; 139/2; 181/1; 212/3; 273/2; 298/1
C; Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
C; Keywords: acyltransferase; coenzyme A; cysteine biosynthesis
C; Keywords: serine acetyltransferase homology <SAT>
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A;Status: preliminary
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A; Map position: 1
C; Superfamily: serine
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                                                                                                LESALAHILSVKLSNLNLPSNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVH 139
                                                                                                                                                                                                                                                                   FRPGFSVNRK-IHHTQIEDD------DDVWIKMLEEAKSDVKQEPILSNYYYASITSHRS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARIVGRPQS - - - - DK - PSLDMDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTQIEDDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP 98
                                                                                                                                                                                                    FESGFEVYAKGTHKSEFDSNLLDPRSDPIWDAIREEAKLEAEKEPILSSFLYAGILAHDC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTLGGTGKECGDRHPKIREGVMIGAGAKILGNIEVGEGAKIGSGSVVLQAVPPHTTVAGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMAVREVIEEAFAADPSISEAAACDICATVNRDPAVSMYSMPLLYLKGYHALQGYRVANW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTK-----VWQTIVAEAREQAEQEPMLASFYHATIIKHDSLKAALSYILANRLNTASMP
                                                                                                                                                                                                                                                                                                                                                138;
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45.2%;
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Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                              Score 643; DB 2;
Pred. No. 6.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Job time: 26 sec
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R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U32743; GB:L42023; NID:g1573597; PIDN:AAC22265.1; PID:g1573599 C;Superfamily: serine acetyltransferase; serine acetyltransferase; homology C;Keywords: acyltransferase; coencyme A; cysteine biosynthesis F;80-240/Domain: serine acetyltransferase homology <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Hacmophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-May-2000
C;Accession: G64080
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     ENPRKHDKI -- PCLTMDQ 302
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                                                                                                QSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGK 286
                                                                                                                                                LALYLONQISVAFDVDIHPAAKIGHGIMFDHATGIVVGETSVIENDVSILQGVTLGGTGK
                                                                                                                                                                                                VALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK 226
                                                                                                                                                                                                                                                EEAYQSNPSIIDCAACDIQAVRHRDPAVELWSTPLLYLKGFHAIQSYRITHYLWNQNRKS
                                                                                                                                                                                                                                                                                             ISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKI 166
                                                                                                                                                                                                                                                                                                                                                DVWQHIRQEAKELAENEPMLASFFHSTILKHQNLGGALSYLLANKLANPIMPAISLREII 63
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                                                     ESGDRHPKVREGYMIGAGAKILGNIEVGKYAKIGANSVVLNPVPEYATAAGVPARIV---
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54; Mismatches
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